

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/997,610

DATE: 12/10/2001

TIME: 16:20:13

Input Set : A:\00-96 SEQ.txt

Output Set: N:\CRF3\12102001\I997610.raw

ENTERED

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3 <110> APPLICANT: Fox, Brian
4     Holloway, James L.
6 <120> TITLE OF INVENTION: ADIPOCYTE COMPLMENT RELATED PROTEIN
7     ZACRP13
9 <130> FILE REFERENCE: 00-96
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/997,610
C--> 11 <141> CURRENT FILING DATE: 2001-11-29
11 <150> PRIOR APPLICATION NUMBER: US 60/253,924
12 <151> PRIOR FILING DATE: 2000-11-29
14 <160> NUMBER OF SEQ ID NOS: 7
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1381
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (2)...(1381)
27 <400> SEQUENCE: 1
28  g ata gtc gtc ata cct gtc tta ata acg gca gtc att gag cat gta gaa      49
29  ile Val Val Ile Pro Val Leu Ile Thr Ala Val Ile Glu His Val Glu
30      1             5             10             15
32  gtt gct gga cct cca gca cac ccc agg ccc cca gaa gaa gtc ggg cct      97
33  Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
34      20             25             30
36  cct ggt gca cca ggt tta cca caa tat aca gga gaa ata agt gaa atg      145
37  Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
38      35             40             45
40  aca aaa tgc ccc tgt cct gat ata gaa agg tca gcc ttt act gtc aag      193
41  Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
42      50             55             60
44  ctc agt gga aaa ctt cct ctt cct ttc aag ccc atc atc ttc aca ggg      241
45  Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly
46      65             70             75             80
48  gtc ctg tac aat gcc cag agg gat tta aag gag gcc atg gga gtc ttt      289
49  Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe
50      85             90             95
52  gct tgc agg gtg cct ggg aat tac tac tcc agc ttt gat gtt gag ctg      337
53  Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu
54      100            105            110
56  cat cat tgc aag gtg aat att tgg cta atg agg aag caa att ttg gct      385
57  His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala
58      115            120            125
60  aat aag gaa gaa att tct aag cag caa agc att caa gag gtg act tgg      433
61  Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp
62      130            135            140
64  gtg ctg tta aag gca ttc agt ttc ata agg gag gca gag cat aag agt      481

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65	Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	Glu	Ala	Glu	His	Lys	Ser	
66	145					150					155					160	
68	tca	gaa	aat	ttg	cac	cct	gac	aat	gtg	ata	aaa	aag	aaa	aac	cca	ttt	529
69	Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile	Lys	Lys	Lys	Asn	Pro	Phe	
70					165					170						175	
72	tct	gag	ggg	aaa	ttc	aag	ctg	gct	gca	gaa	att	tgc	ata	tgt	aat	gag	577
73	Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu	Ile	Cys	Ile	Cys	Asn	Glu	
74					180					185						190	
76	gag	ctg	aat	gtt	aat	cct	caa	gac	aat	ggg	gaa	aat	atc	tcc	tgg	aca	625
77	Glu	Leu	Asn	Val	Asn	Pro	Gln	Asp	Asn	Gly	Glu	Asn	Ile	Ser	Trp	Thr	
78					195					200						205	
80	tgt	cag	agg	tct	tca	cag	cag	tcc	atc	aaa	tca	ctg	gcc	tgg	agg	cct	673
81	Cys	Gln	Arg	Ser	Ser	Gln	Gln	Ser	Ile	Lys	Ser	Leu	Ala	Trp	Arg	Pro	
82					210					215						220	
84	agg	aga	aaa	tgg	ttt	tgt	ggg	aca	ggc	cca	ggg	tcc	ctg	tgc	tgt	gtg	721
86	Arg	Arg	Lys	Trp	Phe	Cys	Gly	Thr	Gly	Pro	Gly	Ser	Leu	Cys	Cys	Val	
87	225					230					235					240	
89	cag	cct	aga	gac	ttg	gtg	ccc	tgt	gtc	cca	gtt	aat	tca	gct	gtg	gct	769
90	Gln	Pro	Arg	Asp	Leu	Val	Pro	Cys	Val	Pro	Val	Asn	Ser	Ala	Val	Ala	
91					245						250					255	
93	tca	gag	ggt	gca	agc	ccc	aag	cct	tgg	cag	ctt	cca	agt	ggt	gtt	gag	817
94	Ser	Glu	Gly	Ala	Ser	Pro	Lys	Pro	Trp	Gln	Leu	Pro	Ser	Gly	Val	Glu	
95					260						265					270	
97	cct	gtg	ggt	gca	aag	aag	tca	aga	att	gag	gtt	tgg	gaa	cct	cca	atc	865
98	Pro	Val	Gly	Ala	Lys	Lys	Ser	Arg	Ile	Glu	Val	Trp	Glu	Pro	Pro	Ile	
99					275						280					285	
101	aga	ttt	cag	aag	ata	tat	gga	aac	ccc	tgg	atg	ccc	agg	cag	aag	ttt	913
102	Arg	Phe	Gln	Lys	Ile	Tyr	Gly	Asn	Pro	Trp	Met	Pro	Arg	Gln	Lys	Phe	
103					290						295					300	
105	gct	gta	ggg	gtg	ggg	tcc	tca	tgg	aga	acc	tct	gca	agg	gta	gta	caa	961
106	Ala	Val	Gly	Val	Gly	Ser	Ser	Trp	Arg	Thr	Ser	Ala	Arg	Val	Val	Gln	
107	305					310					315					320	
109	aag	gga	aat	gtt	ggg	tgg	gag	ccc	cca	cac	aga	gtc	ccc	agt	ggg	gct	1009
110	Lys	Gly	Asn	Val	Gly	Trp	Glu	Pro	Pro	His	Arg	Val	Pro	Ser	Gly	Ala	
111					325						330					335	
113	cca	tct	agt	aga	gct	gtg	aga	aga	agt	cca	cca	tcc	tcc	aga	ctc	cag	1057
114	Pro	Ser	Ser	Arg	Ala	Val	Arg	Arg	Ser	Pro	Pro	Ser	Ser	Arg	Leu	Gln	
115					340						345					350	
117	aag	ggt	aga	tcc	act	gac	agc	ttg	cag	cat	gtg	cct	gaa	aaa	tcc	aca	1105
118	Lys	Gly	Arg	Ser	Thr	Asp	Ser	Leu	Gln	His	Val	Pro	Glu	Lys	Ser	Thr	
119					355						360					365	
121	gac	act	cag	tgc	cag	cct	gtg	aaa	gca	gca	ggg	atg	gag	tct	gta	ccc	1153
122	Asp	Thr	Gln	Cys	Gln	Pro	Val	Lys	Ala	Ala	Gly	Met	Glu	Ser	Val	Pro	
123					370						375					380	
125	tac	aaa	acc	gta	gtg	gca	gag	ctg	acc	aag	acc	gtg	gga	atc	tac	ctc	1201
126	Tyr	Lys	Thr	Val	Val	Ala	Glu	Leu	Thr	Lys	Thr	Val	Gly	Ile	Tyr	Leu	
127	385					390					395					400	
129	ttg	cat	tgt	cat	gac	ctg	gac	gtg	aga	cat	gga	gtc	aaa	aga	gat	cat	1249
130	Leu	His	Cys	His	Asp	Leu	Asp	Val	Arg	His	Gly	Val	Lys	Arg	Asp	His	

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131          405          410          415
133 ttt gga gct tta aga ttt gac tgc ccc act gga ttt cgg act tat atg      1297
134 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
135          420          425          430
137 ggg ccc gta ccc ctt tgt ttt ggc caa ttt ttt cca ttt gga act gcc      1345
138 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
139          435          440          445
141 gta ttt acc caa tgc ctg tac ctc cat tgt atg tag      1381
142 Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met *
143          450          455
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 459
148 <212> TYPE: PRT
149 <213> ORGANISM: Homo sapiens
151 <400> SEQUENCE: 2
152 Ile Val Val Ile Pro Val Leu Ile Thr Ala Val Ile Glu His Val Glu
153 1 5 10 15
154 Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
155 20 25 30
156 Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
157 35 40 45
158 Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
159 50 55 60
160 Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly
161 65 70 75 80
162 Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe
163 85 90 95
164 Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu
165 100 105 110
166 His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala
167 115 120 125
168 Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp
169 130 135 140
170 Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser
171 145 150 155 160
172 Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe
173 165 170 175
174 Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu
175 180 185 190
176 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr
177 195 200 205
178 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro
179 210 215 220
180 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val
181 225 230 235 240
182 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala
183 245 250 255
184 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu
185 260 265 270

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```

186 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile
187           275                      280                      285
188 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe
189           290                      295                      300
190 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln
191           305                      310                      315                      320
192 Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala
193           325                      330                      335
194 Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln
195           340                      345                      350
196 Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr
197           355                      360                      365
198 Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro
199           370                      375                      380
200 Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu
201           385                      390                      395                      400
202 Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His
203           405                      410                      415
204 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
205           420                      425                      430
206 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
207           435                      440                      445
208 Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met
209           450                      455

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211 <210> SEQ ID NO: 3

212 <211> LENGTH: 1377

213 <212> TYPE: DNA

214 <213> ORGANISM: Artificial Sequence

216 <220> FEATURE:

217 <223> OTHER INFORMATION: Degenerate polynucleotide encoding a polypeptide
 218 of SEQ ID NO:2

220 <221> NAME/KEY: variation

221 <222> LOCATION: (1)...(1377)

222 <223> OTHER INFORMATION: Each n is independently A, T, G, or C.

224 <221> NAME/KEY: misc_feature

225 <222> LOCATION: (1)...(1377)

226 <223> OTHER INFORMATION: n = A,T,C or G

228 <400> SEQUENCE: 3

```

W--> 229 athgtngtna thcngtnyt nathacngcn gtnathgarc aygtngargt ngcnggncn      60
W--> 230 ccngcncayc cnmgncncnc ngargargtn ggncncncng gngcncncng nytnccncar      120
W--> 231 tayaacngng arathwsnga ratgacnaar tgyccntgyc cngayathga rmgnwsngcn      180
W--> 232 ttyacngtna arytnwsngg naarytnccn ytnccnttya arccnathat httyacnggn      240
W--> 233 gtnytnaya aygcncarmg ngayytnaar gargcnatgg gngtnttygc ntgygmngtn      300
W--> 234 ccnggnaayt aytaywsnws nttygaygtn garytncayc aytgyaargt naayathtg      360
W--> 235 ytnatgmnga arcarathyt ngcnaayaar gargarathw snaarcarca rwsnathcar      420
W--> 236 gargtnacnt gggtnytnyt naargcntty wsnttyathm gngargcnga rcayaarwsn      480
W--> 237 wsngaraayy tncayccnga yaaygtnath aaraaraara ayccnttyws ngarggnaar      540
W--> 238 ttyaarytng cngcngarat htgyathtg yaygargary tnaaygtnaa yccncargay      600
W--> 239 aayggngara ayathwsntg gacntgyar mgnwsnwsnc arcarwsnat haarwsnytn      660

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W--> 240  gcntggmgnc  cnmgnmgnaa  rtgggttytgy  ggnacnggnc  cnggnwsnyt` ntgytgygtn      720
W--> 241  carccnmngn  ayytngtncc  ntgygtncn  gtnaaywsng  cngtngcnws  ngarggngcn      780
W--> 242  wsnccnaarc  cntggcaryt  nccnwsngn  gtngarccng  tnggngcnaa  raarwsnmgn      840
W--> 243  athgargtnt  gggarccncc  nathmgntty  caraaratht  ayggnaaycc  ntggatgccn      900
W--> 244  mgncaraart  tygcngtngg  ngtnngnwsn  wsntggmgna  cnwsngcnmg  ngtngtncar      960
W--> 245  aarggnaayg  tnggntggga  rcnccncay  mgngtnccnw  snggngcncc  nwsnwsnmgn     1020
W--> 246  gcngtnmgnm  gnwsnccncc  nwsnwsnmgn  ytncaraarg  gnmgnwsnac  ngaywsnytn     1080
W--> 247  carcaygtnc  cngaraarws  nacngayacn  cartgycarc  cngtnaargc  ngcnggnatg     1140
W--> 248  garwsngtnc  cntayaarac  ngtngtngcn  garytnacna  aracngtngg  nathtayytn     1200
W--> 249  ytncaytgyc  aygayytnga  ygtnmgnca  ggngtnaarm  gngaycaytt  yggngcnytn     1260
W--> 250  mgnttygayt  gyccnacngg  nttymgnacn  tayatgggnc  cngtnccnyt  ntgyttyggg     1320
W--> 251  carttytytc  cnttyggnac  ngcngtntty  acncartggy  tntayytnca  ytgyatg        1377

253 <210> SEQ ID NO: 4
254 <211> LENGTH: 31
255 <212> TYPE: PRT
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Aromatic motif
261 <221> NAME/KEY: VARIANT
262 <222> LOCATION: (2)...(6)
263 <223> OTHER INFORMATION: Each Xaa is any amino acid residue
265 <221> NAME/KEY: VARIANT
266 <222> LOCATION: (7)...(7)
267 <223> OTHER INFORMATION: Xaa is asparagine or aspartic acid
269 <221> NAME/KEY: VARIANT
270 <222> LOCATION: (8)...(11)
271 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
273 <221> NAME/KEY: VARIANT
274 <222> LOCATION: (12)...(12)
275 <223> OTHER INFORMATION: Xaa is phenylalanine, tyrosine, tryptophan, or
276     leucine
279 <221> NAME/KEY: VARIANT
280 <222> LOCATION: (13)...(18)
281 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
283 <221> NAME/KEY: VARIANT
284 <222> LOCATION: (20)...(24)
285 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
287 <221> NAME/KEY: VARIANT
288 <222> LOCATION: (26)...(26)
289 <223> OTHER INFORMATION: Xaa is any amino acid residue
291 <221> NAME/KEY: VARIANT
292 <222> LOCATION: (28)...(31)
293 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
295 <400> SEQUENCE: 4
W--> 296  Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
297      1              5              10              15
W--> 298  Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Xaa Xaa Xaa
299              20              25              30
301 <210> SEQ ID NO: 5

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VERIFICATION SUMMARY

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Input Set : A:\00-96 SEQ.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

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L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

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L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

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L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7